Amendments to the Specification:

Please replace paragraph **[0009]** beginning at page 3, line 1, with the following:

--**[0009]** The invention also provides a method for determining the presence or absence of a colorectal cancer cell in a patient, by determining the level of a target nucleic acid that encodes the Copine 1 (CPNE 1) protein, the Integrin B4 binding protein (ITGB4BP), RNA Export homolog (RAE1), bone ~~morphogenic~~ morphogenetic protein 7 (BMP7), G protein, alpha stimulating activity polypeptide 1 (GNAS), eukaryotic translation initiation factor 2, subunit 2 beta (EIF2S2), dynein light chain A2 (DNCL2A), ~~proteosome~~ proteasome subunit α-7 (PSMA7), activity dependent ~~neuroprotector~~ neuroprotective protein (ADNP), C20orf129, C20orf52, C20orf20, or C20orf188 (*e.g.*, SEQ ID NO:4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28) in a biological sample from the patient. In one embodiment, the target nucleic acid comprises a sequence at least 80% identical to SEQ ID NO:3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27. In a further embodiment, the biological sample can include isolated nucleic acids. In another embodiment, the nucleic acids are amplified before the level of the target nucleic acid is determined. In an additional embodiment the isolated nucleic acids are mRNA.--

Please replace paragraph **[0024]** beginning at page 7, line 19, with the following:

--**[0024]** The terms "bone ~~morphogenic~~ morphogenetic protein 7 (BMP7) protein" or "bone ~~morphogenic~~ morphogenetic protein 7 (BMP7) polynucleotide" or refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues of SEQ ID NO: 9 or SEQ ID NO: 10. Typically such genes or proteins have a sequence that has greater than about 70% nucleotide sequence identity, usually 80%, 85%, 90% or 99% or greater sequence identity to SEQ ID NO: 9 or SEQ ID NO: 10, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more residues. A polynucleotide or polypeptide sequence

is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. These terms include both naturally occurring or recombinant forms.--

Please replace paragraph **[0028]** beginning at page 8, line 28, with the following:

--**[0028]** The terms "~~proteosome~~ proteasome subunit α-7 (PSMA7) protein" or "~~proteosome~~ proteasome subunit α-7 (PSMA7) polynucleotide" or refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues of SEQ ID NO: 17 or SEQ ID NO: 18. Typically such genes or proteins have a sequence that has greater than about 70% nucleotide sequence identity, usually 80%, 85%, 90% or 99% or greater sequence identity to SEQ ID NO: 17 or SEQ ID NO: 18, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more residues. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. These terms include both naturally occurring or recombinant forms.--

Please replace paragraph **[0029]** beginning at page 9, line 6, with the following:

--**[0029]** The terms "activity dependent ~~neuroprotector~~ neuroprotective protein (ADNP) ~~protein~~" or "activity dependent ~~neuroprotector~~ neuroprotective protein (ADNP) polynucleotide" ~~or~~ refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues of SEQ ID NO: 19 or SEQ ID NO: 20. Typically such genes or proteins have a sequence that has greater than about 70% nucleotide sequence identity, usually 80%, 85%, 90% or 99% or greater sequence identity to SEQ ID NO: 19 or SEQ ID NO: 20, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more residues. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to,

primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. These terms include both naturally occurring or recombinant forms.--

Please replace paragraph **[0146]** beginning at page 41, line 15, with the following:

--**[0146]** Thirteen additional genes that reside on the q-arm of chromosome 20 are amplified in approximately 60% of human colorectal cancers and have concurrent upregulation of their RNA. Most genes in colorectal cancer amplicons downregulate their RNA to maintain normal levels. These thirteen genes do not, and are therefore upregulated at both the DNA and RNA level and may contribute to the cancer phenotype; *i.e.*, they may be targets of the amplification. The thirteen genes encode Copine I (CPN1), Integrin beta-4 binding protein (ITGB4BP), RNA Export I (RAE1), Bone ~~morphogenic~~ morphogenetic protein 7 (BMP7), GTP-binding protein, alpha-stimulatory (GNAS), eukaryotic translation initiation factor 2, subunit 2 (EIF2S2), Dynein ligt chain A2, (DNCL2A), ~~Proteosome~~ Proteasome subnit alpha-type 7 (PSMA7), Activity dependent ~~neuroprotector~~ neuroprotective protein (ADNP), C20ORF129, C20ORF52, C20ORF20, and C20ORF188. Accession numbers for the genes are found in Figure 2.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1-30, at the end of the application.

Amendments to the Informal Sequence Listing:

Please replace the title of SEQ ID NO:17 at page 47, line 35, with the following:

--~~Proteosome~~ Proteasome subunit α-7 (PSMA7) BC004427--

Please replace the title of SEQ ID NO:18 at page 48, line 4, with the following:

--~~Proteosome~~ Proteasome subunit α-7 (PSMA7) BC004427--

Please replace the title of SEQ ID NO:19 at page 48, line 12, with the following:

--Activity ~~dep. Neuroprotector~~ dependent neuroprotective protein (ADNP) AF250860--

Please replace the title of SEQ ID NO:20 at page 49, line 38, with the following:

--Activity ~~dep. Neuroprotector~~ dependent neuroprotective protein (ADNP) AF250860--